

SEQUENCE LISTING

<110> BASF AG

<120> Method for the genetic modification of organisms of the Blakeslea genus,
corresponding organisms and use of the same

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<160> 80

<170> PatentIn version 3.2

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21

<210> 6

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<400> 6

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21

<210> 7

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<213> Artificial

<220>

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<400> 8

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21

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<211> 24

<212> DNA

<213> Artificial

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<223> Primer

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24

<210> 10

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<400> 10

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24

<210> 11

<211> 1771

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (166)..(1155)

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120

ccgcgagtct cccgccgcac tgactgccat agcacagcta gacga atg cag cta gca

177

Met Gln Leu Ala

1

gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag

225

Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys	
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gag aag gag aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg	273
Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp	
25 30 35	
gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg	321
Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro	
40 45 50	
gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc	369
Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile	
55 60 65	
aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac	417
Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His	
70 75 80	
gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg	465
Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp	
85 90 95 100	
ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc	513
Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser	
105 110 115	
ctg ctc gac atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca	561
Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr	
120 125 130	
ggc ctt ttt atc acc acg cat gat gct atg cat ggc acc atc gcc atg	609
Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met	
135 140 145	
aga aac agg cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg	657
Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu	
150 155 160	
tac gcc tgg ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac	705
Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His	
165 170 175 180	

cac aac cac act ggc gag gtg ggc aag gac cct gac ttc cac agg gga	753
His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly	
185 190 195	
aac cct ggc att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg	801
Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met	
200 205 210	
tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag	849
Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln	
215 220 225	
ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg	897
Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala	
230 235 240	
ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc	945
Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro	
245 250 255 260	
cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg	993
His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met	
265 270 275	
aac tgg tgg aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt	1041
Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe	
280 285 290	
ctg acc tgc tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc	1089
Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro	
295 300 305	
ttc gcc ccc tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga	1137
Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg	
310 315 320	
ggc ctg gtt cct gcc tag ctggacacac tgcagtgggc cctgctgcca	1185
Gly Leu Val Pro Ala	
325	
gctgggcatg cagggtgtgg caggactggg tgaggtgaaa agctgcaggc gctgctgccc	1245

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<210> 12

<211> 329

<212> PRT

<213> Haematococcus pluvialis

<400> 12

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Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
85 90 95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
100 105 110

Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
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Leu Ser Gly Arg Gly Leu Val Pro Ala
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<210> 13
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<212> DNA
<213> Haematococcus pluvialis

<220>
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ctccgctcctc tgccaaatct cgcgtcgggg cctgcctaag tcgaaga atg cac gtc	176
Met His Val	
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gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc	224
Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser	
5 10 15	
agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc	272
Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser	
20 25 30 35	
gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct	320
Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro	
40 45 50	
cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc	368
Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly	
55 60 65	
acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg	416
Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro	
70 75 80	
aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc	464
Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala	
85 90 95	
cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc	512
Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe	
100 105 110 115	
att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac	560
Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp	
120 125 130	
gca atg cat ggc acc ata gct ttg agg cac agg cag ctc aat gat ctc	608
Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu	
135 140 145	
ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac tac agc atg	656

Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met	
150 155 160	
ctg cat cgc aag cac tgg gag cac cac aac cat act ggc gaa gtg ggg	704
Leu His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly	
165 170 175	
aaa gac cct gac ttc cac aag gga aat ccc ggc ctt gtc ccc tgg ttc	752
Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe	
180 185 190 195	
gcc agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg	800
Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu	
200 205 210	
gca tgg tgg gca gtg gtg atg caa atg ctg ggg gcg ccc atg gca aat	848
Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn	
215 220 225	
ctc cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc	896
Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu	
230 235 240	
ttc tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca	944
Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala	
245 250 255	
gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca	992
Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala	
260 265 270 275	
tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg	1040
Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp	
280 285 290	
gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc	1088
Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys	
295 300 305	
cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga	1130
Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala	
310 315 320	

cctgggccct ccgctgggtga cccagcgtct gcacaagagt gtcattgctac aggggtgctgc 1190
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<210> 14

<211> 320

<212> PRT

<213> *Haematococcus pluvialis*

<400> 14

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 20 25 30

Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala
 35 40 45

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
 50 55 60

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
65 70 75 80

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
85 90 95

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
100 105 110

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
115 120 125

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu
130 135 140

Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
145 150 155 160

Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly
165 170 175

Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val
180 185 190

Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe
195 200 205

Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro
210 215 220

Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala
 225 230 235 240

Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro
 245 250 255

Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr
 260 265 270

Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp
 275 280 285

Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu
 290 295 300

Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala
 305 310 315 320

<210> 15

<211> 729

<212> DNA

<213> Agrobacterium aurantiacum

<220>

<221> CDS

<222> (1)..(729)

<400> 15

atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc acc agc ctg 48
 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat 96
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca	144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	
35 40 45	
aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
50 55 60	
cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat	240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	
65 70 75 80	
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	
gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	
115 120 125	
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
130 135 140	
gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac	480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	
145 150 155 160	
gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc	528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
165 170 175	
gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	
180 185 190	
gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg	624

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac 672
 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720
 Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

acc gca tga 729
 Thr Ala

<210> 16
 <211> 242
 <212> PRT
 <213> Agrobacterium aurantiacum

<400> 16

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225 230 235 240

Thr Ala

<210> 17

<211> 1631

<212> DNA

<213> Alcaligenes sp.

<220>

<221> CDS

<222> (99)..(827)

<400> 17

ctgcaggccg ggcccgggtgg ccaatggtcg caaccggcag gactggaaca ggacggcggg 60

ccgggtctagg ctgtcgccct acgcagcagg agtttcgg atg tcc gga cgg aag cct 116

Met Ser Gly Arg Lys Pro

1

5

ggc aca act ggc gac acg atc gtc aat ctc ggt ctg acc gcc gcg atc 164

Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile

10

15

20

ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212

Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp

25

30

35

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260

Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr

40

45

50

tgg ctg tcg gtc ggg ctg ttc atc atc gcg cat gac gca atg cac ggg 308

Trp Leu Ser Val Gly Leu Phe Ile Ile Ala His Asp Ala Met His Gly

55

60

65

70

tcc gtg gtg ccg ggg cgg ccg cgc gcc aat gcg gcg atc ggg caa ctg 356

Ser Val Val Pro Gly Arg Pro Arg Ala Asn Ala Ala Ile Gly Gln Leu

75

80

85

gcg ctg tgg ctc tat gcg ggg ttc tcg tgg ccc aag ctg atc gcc aag 404

Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp Pro Lys Leu Ile Ala Lys	
90 95 100	
cac atg acg cat cac cgg cac gcc ggc acc gac aac gat ccc gat ttc	452
His Met Thr His His Arg His Ala Gly Thr Asp Asn Asp Pro Asp Phe	
105 110 115	
ggt cac gga ggg ccc gtg cgc tgg tac ggc agc ttc gtc tcc acc tat	500
Gly His Gly Gly Pro Val Arg Trp Tyr Gly Ser Phe Val Ser Thr Tyr	
120 125 130	
ttc ggc tgg cga gag gga ctg ctg cta ccg gtg atc gtc acc acc tat	548
Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro Val Ile Val Thr Thr Tyr	
135 140 145 150	
gcg ctg atc ctg ggc gat cgc tgg atg tat gtc atc ttc tgg ccg gtc	596
Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr Val Ile Phe Trp Pro Val	
155 160 165	
ccg gcc gtt ctg gcg tcg atc cag att ttc gtc ttc gga act tgg ctg	644
Pro Ala Val Leu Ala Ser Ile Gln Ile Phe Val Phe Gly Thr Trp Leu	
170 175 180	
ccc cac cgc ccg gga cat gac gat ttt ccc gac cgg cac aac gcg agg	692
Pro His Arg Pro Gly His Asp Asp Phe Pro Asp Arg His Asn Ala Arg	
185 190 195	
tcg acc ggc atc ggc gac ccg ttg tca cta ctg acc tgc ttc cat ttc	740
Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu Leu Thr Cys Phe His Phe	
200 205 210	
ggc ggc tat cac cac gaa cat cac ctg cat ccg cat gtg ccg tgg tgg	788
Gly Gly Tyr His His Glu His His Leu His Pro His Val Pro Trp Trp	
215 220 225 230	
cgc ctg cct cgt aca cgc aag acc gga ggc cgc gca tga cgcaattcct	837
Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly Arg Ala	
235 240	
cattgtcgtg gcgacagtcc tcgtgatgga gctgaccgcc tattccgtcc accgctggat	897
tatgcacggc cccctaggct ggggctggca caagtcccat cacgaagagc acgaccacgc	957

gttggagaag aacgacctct acggcgctcgt cttcgcggtg ctggcgacga tcctcttcac 1017
 cgtggggcgcc tattggtggc cggcgctgtg gtggatcgcc ctgggcatga cggctctatgg 1077
 gttgatctat ttcatactgc acgacgggct tgtgcatcaa cgctggccgt ttcggtatat 1137
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 ggggcgggac cactgcgtca gcttcggctt catctatgcc ccaccgtgg acaagctgaa 1257
 gcaggatctg aagcggtcgg gtgtcctgcg cccccaggac gagcgccgt cgtgatctct 1317
 gatccccggcg tggccgcatg aaatccgacg tgctgctggc aggggcccgc cttgccaacg 1377
 gactgatcgc gctggcgatc cgcaaggcgc ggcccgaact tcgctgtctg ctgctggacc 1437
 gtgcggcggg cgctcggac gggcatactt ggtcctgcca cgacaccgat ttggcgccgc 1497
 actggctgga ccgcctgaag ccgatcaggc gtggcgactg gcccgatcag gaggtgcggt 1557
 tcccagacca ttcgcgaagg ctccgggccg gatatggctc gatcgacggg cgggggctga 1617
 tgcgtgcggt gacc 1631

<210> 18

<211> 242

<212> PRT

<213> Alcaligenes sp.

<400> 18

Met Ser Gly Arg Lys Pro Gly Thr Thr Gly Asp Thr Ile Val Asn Leu
 1 5 10 15

Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
 20 25 30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
35 40 45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
100 105 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
115 120 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
 225 230 235 240

Arg Ala

<210> 19
 <211> 729
 <212> DNA
 <213> *Paracoccus marcusii*

<220>
 <221> CDS
 <222> (1)..(729)

<400> 19
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 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15
 atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat 96
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30
 gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg 144
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
 35 40 45
 aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60
 cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat 240

His	Asp	Ala	Met	His	Gly	Ser	Val	Val	Pro	Gly	Arg	Pro	Arg	Ala	Asn	
65						70					75				80	
gcg	gcg	atg	ggc	cag	ctt	gtc	ctg	tgg	ctg	tat	gcc	gga	ttt	tcg	tgg	288
Ala	Ala	Met	Gly	Gln	Leu	Val	Leu	Trp	Leu	Tyr	Ala	Gly	Phe	Ser	Trp	
			85						90				95			
cgc	aag	atg	atc	gtc	aag	cac	atg	gcc	cat	cac	cgc	cat	gcc	gga	acc	336
Arg	Lys	Met	Ile	Val	Lys	His	Met	Ala	His	His	Arg	His	Ala	Gly	Thr	
			100					105					110			
gac	gac	gac	cca	gat	ttc	gac	cat	ggc	ggc	ccg	gtc	cgc	tgg	tac	gcc	384
Asp	Asp	Asp	Pro	Asp	Phe	Asp	His	Gly	Gly	Pro	Val	Arg	Trp	Tyr	Ala	
		115					120					125				
cgc	ttc	atc	ggc	acc	tat	ttc	ggc	tgg	cgc	gag	ggg	ctg	ctg	ctg	ccc	432
Arg	Phe	Ile	Gly	Thr	Tyr	Phe	Gly	Trp	Arg	Glu	Gly	Leu	Leu	Leu	Pro	
	130					135				140						
gtc	atc	gtg	acg	gtc	tat	gcg	ctg	atc	ctg	ggg	gat	cgc	tgg	atg	tac	480
Val	Ile	Val	Thr	Val	Tyr	Ala	Leu	Ile	Leu	Gly	Asp	Arg	Trp	Met	Tyr	
145					150				155					160		
gtg	gtc	ttc	tgg	ccg	ttg	ccg	tcg	atc	ctg	gcg	tcg	atc	cag	ctg	ttc	528
Val	Val	Phe	Trp	Pro	Leu	Pro	Ser	Ile	Leu	Ala	Ser	Ile	Gln	Leu	Phe	
				165				170					175			
gtg	ttc	ggc	act	tgg	ctg	ccg	cac	cgc	ccc	ggc	cac	gac	gcg	ttc	ccg	576
Val	Phe	Gly	Thr	Trp	Leu	Pro	His	Arg	Pro	Gly	His	Asp	Ala	Phe	Pro	
			180					185					190			
gac	cgc	cat	aat	gcg	cgg	tcg	tcg	cgg	atc	agc	gac	cct	gtg	tcg	ctg	624
Asp	Arg	His	Asn	Ala	Arg	Ser	Ser	Arg	Ile	Ser	Asp	Pro	Val	Ser	Leu	
		195					200					205				
ctg	acc	tgc	ttt	cat	ttt	ggc	ggt	tat	cat	cac	gaa	cac	cac	ctg	cac	672
Leu	Thr	Cys	Phe	His	Phe	Gly	Gly	Tyr	His	His	Glu	His	His	Leu	His	
	210					215					220					
ccg	acg	gtg	ccg	tgg	tgg	cgc	ctg	ccc	agc	acc	cgc	acc	aag	ggg	gac	720
Pro	Thr	Val	Pro	Trp	Trp	Arg	Leu	Pro	Ser	Thr	Arg	Thr	Lys	Gly	Asp	
225					230				235						240	

acc gca tga

729

Thr Ala

<210> 20

<211> 242

<212> PRT

<213> Paracoccus marcusii

<400> 20

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu

1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His

20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala

35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala

50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn

65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp

85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr

100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala

115

120

125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225 230 235 240

Thr Ala

<210> 21

<211> 1629

<212> DNA

<213> Synechocystis sp.

<222> (1) . . (1629)

atg atc acc acc gat gtt gtc att att ggg gcg ggg cac aat ggc tta 48
Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu
1 5 10 15

gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta 96
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
20 25 30

gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg 144
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met..
35 40 45

ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac 192
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
50 55 60

gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag 240
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
65 70 75 80

tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg 288
Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
85 90 95

ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt 336
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
100 105 110

gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa 384
Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
115 120 125

ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt 432
Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
130 135 140

caa ttg gtg gaa ccg ggg gcc cta gcc aag gtg aat caa aac cta ggg 960

Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
65 70 75 80

Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
85 90 95

Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
100 105 110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
115 120 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
130 135 140

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
145 150 155 160

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
165 170 175

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
180 185 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
195 200 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
210 215 220

Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
225 230 235 240

Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
245 250 255

Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
260 265 270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
275 280 285

Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
290 295 300

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
305 310 315 320

Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
325 330 335

Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
340 345 350

Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
355 360 365

Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
450 455 460

Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
500 505 510

Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
515 520 525

Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
530 535 540

<210> 23

<211> 776

<212> DNA

<213> Bradyrhizobium sp.

<220>

<221> CDS

<222> (1)..(774)

<400> 23

atg cat gca gca acc gcc aag gct act gag ttc ggg gcc tct cgg cgc 48
 Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
 1 5 10 15

gac gat gcg agg cag cgc cgc gtc ggt ctc acg ctg gcc gcg gtc atc 96
 Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
 20 25 30

atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg 144
 Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
 35 40 45

ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag 192
 Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
 50 55 60

acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac 240
 Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
 65 70 75 80

ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag 288
 Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95

ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc 336
 Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat 384
 Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
 115 120 125

ttc gac gag gtg ccg ccg cac ggc ttc tgg cac tgg ttc gcc agc ttt 432
 Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

ttc ctg cac tat ttc ggc tgg aag cag gtc gcg atc atc gca gcc gtc 480
 Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
 145 150 155 160

tcg ctg gtt tat cag ctc gtc ttc gcc gtt ccc ttg cag aac atc ctg 528
 Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
 165 170 175

ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc 576
 Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
 180 185 190

ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat 624
 Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg 672
 Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat 720
 Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

gcg ccg tgg tgg cgg ctg ccg gag atc aag cgg cgg gcc ctg gaa agg 768
 Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

cgt gac ta 776
 Arg Asp

<210> 24

<211> 258

<212> PRT

<213> Bradyrhizobium sp.

<400> 24

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg

1 5 10 15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
 20 25 30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
 35 40 45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
 50 55 60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
 115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
 165 170 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
 180 185 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

Arg Asp

<210> 25
 <211> 777
 <212> DNA
 <213> Nostoc sp.

<220>
 <221> CDS
 <222> (1)..(777)

<400> 25
 atg gtt cag tgt caa cca tca tct ctg cat tca gaa aaa ctg gtg tta 48
 Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

ttg tca tcg aca atc aga gat gat aaa aat att aat aag ggt ata ttt 96
 Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe

20	25	30	
att gcc tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta			144
Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu			
35	40	45	
ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc			192
Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala			
50	55	60	
atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat			240
Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His			
65	70	75	80
gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat			288
Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn			
85	90	95	
ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa			336
Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys			
100	105	110	
gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat			384
Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp			
115	120	125	
tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg			432
Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp			
130	135	140	
tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga			480
Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly			
145	150	155	160
tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa			528
Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu			
165	170	175	
aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta			576
Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val			
180	185	190	

caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt 624
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205

ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt 672
 Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac 720
 Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
 225 230 235 240

gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata 768
 Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
 245 250 255

tct tta taa 777
 Ser Leu

<210> 26
 <211> 258
 <212> PRT
 <213> Nostoc sp.

<400> 26

Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
65 70 75 80

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
100 105 110

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
115 120 125

Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
130 135 140

Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
145 150 155 160

Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
165 170 175

Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
180 185 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
195 200 205

Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
210 215 220

Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
 225 230 235 240

Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
 245 250 255

Ser Leu

<210> 27

<211> 789

<212> DNA

<213> Nostoc punctiforme

<220>

<221> CDS

<222> (1) .. (789)

<400> 27

ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa 48
 Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
 1 5 10 15

tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta 96
 Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
 20 25 30

att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat 144
 Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
 35 40 45

tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa 192
 Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60

atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat 240
 Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His

65	70	75	80	
ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca				288
Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser				
	85	90	95	
cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag				336
Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys				
	100	105	110	
aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat				384
Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp				
	115	120	125	
ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc				432
Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe				
	130	135	140	
atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta				480
Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu				
	145	150	155	160
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc				528
Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile				
	165	170	175	
tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat				576
Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr				
	180	185	190	
ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat				624
Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr				
	195	200	205	
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc				672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile				
	210	215	220	
gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat				720
Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His				
	225	230	235	240

gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac 768
 Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
 245 250 255

aat tca gta acc aat tcg taa 789
 Asn Ser Val Thr Asn Ser
 260

<210> 28

<211> 262

<212> PRT

<213> Nostoc punctiforme

<400> 28

Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
 1 5 10 15

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
 20 25 30

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
 35 40 45

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
 65 70 75 80

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
130 135 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
245 250 255

Asn Ser Val Thr Asn Ser
260

<210> 29
<211> 762
<212> DNA
<213> Nostoc punctiforme

<220>
<221> CDS
<222> (1)..(762)

<400> 29

gtg atc cag tta gaa caa cca ctc agt cat caa gca aaa ctg act cca 48
Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
1 5 10 15

gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96
Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
20 25 30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144
Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
35 40 45

atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa 192
Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
50 55 60

aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240
Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
65 70 75 80

ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288
Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
85 90 95

ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa 336
Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
100 105 110

aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat 384
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
115 120 125

ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt 432
Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
130 135 140

atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att 480
Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
145 150 155 160

tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act 528
Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
165 170 175

tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat 576
Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
180 185 190

ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag 624
Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
195 200 205

cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc 672
Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
210 215 220

acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat 720
Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225 230 235 240

att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag 762
Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
245 250

<210> 30

<211> 253

<212> PRT

<213> Nostoc punctiforme

<400> 30

Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
1 5 10 15

Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
20 25 30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
35 40 45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
50 55 60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
85 90 95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
100 105 110

Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
115 120 125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
130 135 140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr

165

170

175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
 210 215 220

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
 245 250

<210> 31

<211> 1608

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (3)..(971)

<400> 31

ct aca ttt cac aag ccc gtg agc ggt gca agc gct ctg ccc cac atc
 Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
 1 5 10 15

47

ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
 20 25 30

95

tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc	143
Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala	
35 40 45	
cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg	191
Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser	
50 55 60	
tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga	239
Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly	
65 70 75	
acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca	287
Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala	
80 85 90 95	
ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa	335
Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys	
100 105 110	
cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc	383
Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly	
115 120 125	
gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac	431
Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His	
130 135 140	
atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc	479
Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu	
145 150 155	
ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat	527
Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr	
160 165 170 175	
gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac	575
Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His	
180 185 190	
aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg	623
Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu	

195	200	205	
ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc			671
Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly			
210	215	220	
ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg			719
Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu			
225	230	235	
ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg			767
Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu			
240	245	250	255
gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg			815
Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met			
260	265	270	
aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt			863
Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly			
275	280	285	
ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att			911
Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile			
290	295	300	
cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg			959
Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp			
305	310	315	
tcc aag cgg tag ggtgcggaac caggcacgct ggtttcacac ctcatgcctg			1011
Ser Lys Arg			
320			
tgataaggtg tggctagagc gatgcgtgtg agacgggtat gtcacggtcg actggctctga			1071
tggccaatgg catcggccat gtctgggtcat cacgggctgg ttgcctgggt gaaggtgatg			1131
cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc			1191
caggctggcg ttgaatcagt gagggtttgt gattggcggg tgtgaagcaa tgactccgcc			1251

catattctat ttgtgggagc tgagatgatg gcatgcttgg gatgtgcatg gatcatggta 1311
 gtgcagcaaa ctatattcac ctagggtgtg ttgtaggatc aggtgaggcc ttgcacattg 1371
 catgatgtac tcgtcatggg gtgttggtga gaggatggat gtggatggat gtgtattctc 1431
 agacgtagac cttgactgga ggcttgatcg agagagtggg ccgtattctt tgagagggga 1491
 ggctcgtgcc agaaatgggtg agtggatgac tgtgacgctg tacattgcag gcaggtgaga 1551
 tgcactgtct cgattgtaaa atacattcag atgcaaaaaa aaaaaaaaaa aaaaaaa 1608

<210> 32

<211> 322

<212> PRT

<213> Haematococcus pluvialis

<400> 32

Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile Gly
 1 5 10 15

Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser
 20 25 30

Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg
 35 40 45

Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu
 50 55 60

Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr
 65 70 75 80

Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu
 85 90 95

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg
100 105 110

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val
115 120 125

Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met
130 135 140

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu
145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala
165 170 175

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys
180 185 190

Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe
195 200 205

Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe
210 215 220

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly
225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val
245 250 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys
 260 265 270

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
 275 280 285

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
 290 295 300

Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
 305 310 315 320

Lys Arg

<210> 33

<211> 528

<212> DNA

<213> Erwinia uredovora

<220>

<221> CDS

<222> (1)..(528)

<400> 33

atg ttg tgg att tgg aat gcc ctg atc gtt ttc gtt acc gtg att ggc 48
 Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Ile Gly
 1 5 10 15

atg gaa gtg att gct gca ctg gca cac aaa tac atc atg cac ggc tgg 96
 Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
 20 25 30

ggc tgg gga tgg cat ctt tca cat cat gaa ccg cgt aaa ggc gcg ttt 144
 Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
 35 40 45

gaa gtt aac gat ctt tat gcc gtg gtt ttt gct gca tta tcg atc ctg 192
 Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu
 50 55 60

ctg att tat ctg ggc agt aca gga atg tgg ccg ctc cag tgg att ggc 240
 Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
 65 70 75 80

gca ggt atg acg gcg tat gga tta ctc tat ttt atg gtg cac gac ggc 288
 Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
 85 90 95

ctg gtg cat caa cgt tgg cca ttc cgc tat att cca cgc aag ggc tac 336
 Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
 100 105 110

ctc aaa cgg ttg tat atg gcg cac cgt atg cat cac gcc gtc agg ggc 384
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gcgattaagt tgggtaacgc cagggttttc ccagtcacga cgttgtaaaa cgacggccag 16080
tgaattcgag ctcggtaccc ggg 16103

<210> 63
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 63
ggcgtacttg aaggaaccct taccg 25

<210> 64
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 64
attgatgctc ccggtcaccg tgatt 25

<210> 65
<211> 500
<212> DNA

<213> Blakeslea trispora

<400> 65

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gtagagcaac tacaaaagtt agcagagaag catgatttct taatctttga agaccgcaag 120
tttgcagata tcggtatgtg aattctatct attttttttc tgatgtgtgc atggatgact 180
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tcaaggtgca ttaactaagg gtatttacac tgccgaatct gtcaatatgg ctgcccgcaa 420
caaagatttc gtttttggct ttattgcaca acacaaaatg aatcagtatg atgatgagga 480
ttttgttgtc atgtcgctg 500

<210> 66

<211> 611

<212> DNA

<213> Blakeslea trispora

<400> 66

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atatacaagc aatcttcttc aaggagtttg aaattttgtc ctccaggagc aaaaaaaagt 180
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gacagtatct ttgattacac tctaaatctc gatgacccga ccaaaaagag cgaacaaaga 480
aataatcttg tgcattcgaa tatgatggaa gattttttcc cccttattct aaatgttgac 540
atagcgtgta tggtatataa acaaaaagaa attgtacaaa ctttcttttc ttctcttttt 600
attttatctc t 611

<210> 67

<211> 720

<212> DNA

<213> Blakeslea trispora

<400> 67

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atgttgatgg ccgcctctac cgcacgatt tgggacaatt atatcgttta tcatcgcgct 180
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catatttctc ttagaacaag cactggcaaa atggtagtac ccgatttacc ttagaagaa 660
tgctgtttt ttactttgat caacacagtc ttggtttttg ctacctgtgc tatagaccgc 720

<210> 68

<211> 1089

<212> DNA

<213> *Blakeslea trispora*

<400> 68

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gatgatctta ctatcagctg ggatatttta cgtaaagcct caaagtcatt ctatactgca	180
tctgccgttt ttccaagtta tgtacgtcaa gacttgggtg ttctctatgc tttctgcaga	240
gctaccgatg acctgtgcga tgatgaatcc aaatctgttc aagaaagaag agaccaatta	300
gatcttactc gacaatttgt tcgtgatctc tttagccaaa agaccagtgc gcctattgtg	360
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gaaaatgatg cttggataat tgaccgtgca cgtgagatgg ggctggtgct acaatacgtt	660
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gttgattag	1089

<210> 69
<211> 611
<212> DNA
<213> *Blakeslea trispora*

<400> 69
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acaagattat ttctttgttc gctctttttg gtcgggtcat cgagatttag agtgtaatca 180
aagatactgt catctcgaga gcgttgacaca ggctgctggt tgccaaattg gatgtttgcc 240
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tataaacttg cagcacgtaa gaccaaagca aattggtaac tattcttggtg taaaaacatg 420
tataaaaaaa aacttttttt tgctcctgga ggacaaaatt tcaaactcct tgaagaagat 480
tgcttgtaaa tctatcatat gcatatatca tatcgatgga aaaagaaagt caggcatgta 540
tttataaaaa gaagaatgtg ccatgcttcc gaatttcttt tcactttctt ttccttatct 600
attttaatct c 611

<210> 70
<211> 882
<212> DNA
<213> *Haematococcus pluvialis*

<400> 70
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atcacgcggc ccaaagtctg cctgcatgct cagcgggtgct cgttagtctg gctgcgagtg 120
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<210> 71

<211> 528

<212> DNA

<213> Erwinia uredovora

<400> 71

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catgaaccgc gtaaagggtgc gtttgaagtt aacgatcttt atgccgtggg ttttgctgca 180
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cgatatgcac acgccgctcag gggcaaagaa ggttgtgttt cttttggctt cctctatgcg 420

ccgccccctgt caaaacttca ggcgacgctc cgggaaagac atggcgctag agcgggcgct 480

gccagagatg cgcagggcg gaggatgag cccgcatccg ggaagtaa 528

<210> 72

<211> 762

<212> DNA

<213> Nostoc sp. PCC73102

<400> 72

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ctgagtttat tactttccct tgacatctca aagctaaaat tttggatggt attgcctggt 180

atactatggc aaacatTTTT atatacggga ttatttatta catctcatga tgccatgcac 240

ggcgtagtat ttccccaaaa caccaagatt aatcatttga ttggaacatt gaccctatcc 300

ctttatggtc ttttaccata tcaaaaacta ttgaaaaaac attgggttaca ccaccacaat 360

ccagcaagct caatagaccc ggattttcac aatggtaaac accaaagttt ctttgcttgg 420

tattttcatt ttatgaaagg ttactggagt tgggggcaaa taattgcgtt gactattatt 480

tataactttg ctaaatacat actccatata ccaagtata atctaactta cttttgggtg 540

ctaccctcgc ttttaagttc attacaatta ttctattttg gtactttttt accccatagt 600

gaaccaatag ggggttatgt tcagcctcat tgtgcccaaa caattagccg tcctatttgg 660

tggtcattta tcacgtgcta tcattttggc taccacgagg aacatcacga atatcctcat 720

atttcttggt ggcagttacc agaaatttac aaagcaaat ga 762

<210> 73

<211> 617

<212> DNA

<213> *Haematococcus pluvialis*

<400> 73

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catgtctggg catcacgggc tgggtgcctg ggtgaagggtg atgcacatca tcatgtgcgg 180

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aaaatacatt cagatgc 617

<210> 74

<211> 1208

<212> DNA

<213> *Haematococcus pluvialis*

<400> 74

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ggcttgtctc tgaagcttgt aggaaaggca gacgctatca tggtgagagc taagaagggc 180

attgacaagt tgccggcaaa ctgtcaaggc ggtgtacgag ctgcttgcca agtatatgct 240

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<210> 75

<211> 6316

<212> DNA

<213> Blakeslea trispora

<220>

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<223> n is a, c, g, or t

<220>
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<222> (4263)..(4263)
<223> n is a, c, g, or t

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<211> 1170

<212> DNA

<213> *Thermus thermophilus*

<400> 76

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<211> 2981

<212> DNA

<213> Blakeslea trispora

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<213> *Blakeslea trispora*

<400> 78

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